

OIEP

RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/810,428

TIME: 16:04:56

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF3\10292001\I810428.raw

3 <110> APPLICANT: HOOK, Magnus
 5 <120> TITLE OF INVENTION: CROSS-REACTIVE DISPLACING ANTIBODIES FROM COLLAGEN-BINDING
 PROTEINS AND

ENTERED

6 METHOD OF IDENTIFICATION AND USE

8 <130> FILE REFERENCE: P06668US03/BAS

10 <140> CURRENT APPLICATION NUMBER: 09/810,428

11 <141> CURRENT FILING DATE: 2001-03-19

13 <150> PRIOR APPLICATION NUMBER: 60/225,402

14 <151> PRIOR FILING DATE: 2000-08-15

16 <150> PRIOR APPLICATION NUMBER: 60/199,370

17 <151> PRIOR FILING DATE: 2000-04-25

19 <150> PRIOR APPLICATION NUMBER: 60/189,968

20 <151> PRIOR FILING DATE: 2000-03-17

22 <160> NUMBER OF SEQ ID NOS: 30

24 <170> SOFTWARE: PatentIn version 3.0

26 <210> SEQ ID NO: 1

27 <211> LENGTH: 336

28 <212> TYPE: DNA

29 <213> ORGANISM: Staphylococcus aureus

31 <400> SEQUENCE: 1

32 gaagttgtga tgacccaaac tccactctcc ctgcctgtca gtcttgccga tcacgcctcc 60

34 atctcttgca gatctagtca ggccttgta cacagtaatg aaaacaccta tttacattgg 120

36 tatctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180

38 tctgggggtcc cagacagggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

40 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac gcatgttcct 300

42 cccacgttcg gaggggggac caggctggaa ataaaa 336

45 <210> SEQ ID NO: 2

46 <211> LENGTH: 112

47 <212> TYPE: PRT

48 <213> ORGANISM: Staphylococcus aureus

50 <400> SEQUENCE: 2

52 Glu Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

53 1 5 10 15

55 Asp His Ala Ser Ile Ser Cys Arg Ser Ser Gln Arg Leu Val His Ser

56 20 25 30

58 Asn Glu Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser

59 35 40 45

61 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

62 50 55 60

64 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 65 70 75 80

67 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser

68 85 90 95

70 Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys

71 100 105 110

73 <210> SEQ ID NO: 3

74 <211> LENGTH: 360

75 <212> TYPE: DNA

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76 <213> ORGANISM: Staphylococcus aureus
78 <400> SEQUENCE: 3
79 cagggttcagc tgcagcagtc tggagctgag ctgatgaagc ctggggcctc agtgaagatc      60
81 tcctgcaagg ctgctggcta cacattcagt ccctactgga tagagtgggt aaagcagagg      120
83 cctggacatg gccttgagtg gattggagag attttacctg gaagtggaaa tattaactac      180
85 aatgagaagt tcaaggacaa ggccacattc actgctgata catcctccaa cacagtttac      240
87 atgcaagtca gcagcctgac atctgaggac tctgccgtct attactgtgc aagagaggag      300
89 gatggttacc cggcctgggt tgcttactgg ggccaaggga ctctggtcac tgtctctgca      360
92 <210> SEQ ID NO: 4
93 <211> LENGTH: 120
94 <212> TYPE: PRT
95 <213> ORGANISM: Staphylococcus aureus
97 <400> SEQUENCE: 4
99 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
100 1          5          10          15
102 Ser Val Lys Ile Ser Cys Lys Ala Ala Gly Tyr Thr Phe Ser Pro Tyr
103          20          25          30
105 Trp Ile Glu Trp Leu Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
106          35          40          45
108 Gly Glu Ile Leu Pro Gly Ser Gly Asn Ile Asn Tyr Asn Glu Lys Phe
109          50          55          60
111 Lys Asp Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
112 65          70          75          80
114 Met Gln Val Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
115          85          90          95
117 Ala Arg Glu Glu Asp Gly Tyr Pro Ala Trp Phe Ala Tyr Trp Gly Gln
118          100         105         110
120 Gly Thr Leu Val Thr Val Ser Ala
121          115         120
123 <210> SEQ ID NO: 5
124 <211> LENGTH: 21
125 <212> TYPE: PRT
126 <213> ORGANISM: Staphylococcus aureus
128 <400> SEQUENCE: 5
130 Ile Thr Ser Gly Asn Lys Ser Thr Asn Val Thr Val His Lys Ser Glu
131 1          5          10          15
133 Ala Gly Thr Ser Ser
134          20
136 <210> SEQ ID NO: 6
137 <211> LENGTH: 115
138 <212> TYPE: PRT
139 <213> ORGANISM: Staphylococcus aureus
141 <400> SEQUENCE: 6
143 Val Phe Tyr Tyr Lys Thr Gly Asp Met Leu Pro Glu Asp Thr Thr His
144 1          5          10          15
146 Val Arg Trp Phe Leu Asn Ile Asn Asn Glu Lys Ser Tyr Val Ser Lys
147          20          25          30
149 Asp Ile Thr Ile Lys Asp Gln Ile Gln Gly Gly Gln Gln Leu Asp Leu
150          35          40          45

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152 Ser Thr Leu Asn Ile Asn Val Thr Gly Thr His Ser Asn Tyr Tyr Ser
153      50              55              60
155 Gly Gln Ser Ala Ile Thr Asp Phe Glu Lys Ala Phe Pro Gly Ser Lys
156 65      70              75              80
158 Ile Thr Val Asp Asn Thr Lys Asn Thr Ile Asp Val Thr Ile Pro Gln
159      85              90              95
161 Gly Tyr Gly Ser Tyr Asn Ser Phe Ser Ile Asn Tyr Lys Thr Lys Thr
162      100             105             110
164 Thr Asn Glu
165      115
167 <210> SEQ ID NO: 7
168 <211> LENGTH: 32
169 <212> TYPE: PRT
170 <213> ORGANISM: Staphylococcus aureus
172 <400> SEQUENCE: 7
174 Gln Gln Lys Glu Phe Val Asn Asn Ser Gln Ala Trp Tyr Gln Glu His
175 1      5              10              15
177 Gly Lys Glu Glu Val Asn Gly Lys Ser Phe Asn His Thr Val His Asn
178      20              25              30
180 <210> SEQ ID NO: 8
181 <211> LENGTH: 37
182 <212> TYPE: PRT
183 <213> ORGANISM: Enterococcus faecalis
185 <400> SEQUENCE: 8
187 Thr Ala Thr Ala Thr Gln Arg Leu Thr Ile Glu Gly Val Thr Asn Thr
188 1      5              10              15
190 Glu Thr Gly Gln Ile Glu Arg Asp Tyr Pro Phe Phe Tyr Lys Val Gly
191      20              25              30
193 Asp Leu Ala Gly Glu
194      35
196 <210> SEQ ID NO: 9
197 <211> LENGTH: 52
198 <212> TYPE: PRT
199 <213> ORGANISM: Enterococcus faecalis
201 <400> SEQUENCE: 9
203 Ser Asn Gln Val Arg Trp Phe Leu Asn Val Asn Leu Asn Lys Ser Asp
204 1      5              10              15
206 Val Thr Glu Asp Ile Ser Ile Ala Asp Arg Gln Gly Ser Gly Gln Gln
207      20              25              30
209 Leu Asn Lys Glu Ser Phe Thr Phe Asp Ile Val Asn Asp Lys Glu Thr
210      35              40              45
212 Lys Tyr Ile Ser
213      50
215 <210> SEQ ID NO: 10
216 <211> LENGTH: 10
217 <212> TYPE: PRT
218 <213> ORGANISM: Enterococcus faecalis
220 <400> SEQUENCE: 10
222 Leu Ala Glu Phe Glu Gln Gln Gly Tyr Gly

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223 1          5          10
225 <210> SEQ ID NO: 11
226 <211> LENGTH: 5
227 <212> TYPE: PRT
228 <213> ORGANISM: Enterococcus faecalis
230 <400> SEQUENCE: 11
232 Lys Ile Asp Phe Val
233 1          5
235 <210> SEQ ID NO: 12
236 <211> LENGTH: 64
237 <212> TYPE: PRT
238 <213> ORGANISM: Enterococcus faecalis
240 <400> SEQUENCE: 12
242 Thr Asp Asn Asp Phe Asn Leu Arg Phe Tyr Arg Asp Lys Ala Arg Phe
243 1          5          10          15
245 Thr Ser Phe Ile Val Arg Tyr Thr Ser Thr Ile Thr Glu Ala Gly Gln
246          20          25          30
248 His Gln Ala Thr Phe Glu Asn Ser Tyr Asp Ile Asn Tyr Gln Leu Asn
249          35          40          45
251 Asn Gln Asp Ala Thr Asn Glu Lys Asn Thr Ser Gln Val Lys Asn Val
252          50          55          60
254 <210> SEQ ID NO: 13
255 <211> LENGTH: 28
256 <212> TYPE: DNA
257 <213> ORGANISM: Staphylococcus aureus
259 <400> SEQUENCE: 13
260 gaagatccat aacatctggg aataaatc
263 <210> SEQ ID NO: 14
264 <211> LENGTH: 27
265 <212> TYPE: DNA
266 <213> ORGANISM: Staphylococcus aureus
268 <400> SEQUENCE: 14
269 gttgtcgact caattgtgca cagtatg
272 <210> SEQ ID NO: 15
273 <211> LENGTH: 25
274 <212> TYPE: DNA
275 <213> ORGANISM: Enterococcus faecalis
277 <400> SEQUENCE: 15
278 gaaggatcca cagcaacggc gactc
281 <210> SEQ ID NO: 16
282 <211> LENGTH: 29
283 <212> TYPE: DNA
284 <213> ORGANISM: Enterococcus faecalis
286 <400> SEQUENCE: 16
287 gttgtcgact caatttttaa cctgtgatg
290 <210> SEQ ID NO: 17
291 <211> LENGTH: 27
292 <212> TYPE: DNA
293 <213> ORGANISM: Enterococcus faecalis

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295 <400> SEQUENCE: 17
296 catgtacgat ggttttttaa tgtgaac 27
299 <210> SEQ ID NO: 18
300 <211> LENGTH: 30
301 <212> TYPE: DNA
302 <213> ORGANISM: Staphylococcus aureus
304 <400> SEQUENCE: 18
305 atttaaaaac catcgtacat gtgtcgtatc 30
308 <210> SEQ ID NO: 19
309 <211> LENGTH: 36
310 <212> TYPE: DNA
311 <213> ORGANISM: Staphylococcus aureus
313 <400> SEQUENCE: 19
314 ttggcctgct tctgtgattt tggttttgta gttaat 36
317 <210> SEQ ID NO: 20
318 <211> LENGTH: 36
319 <212> TYPE: DNA
320 <213> ORGANISM: Enterococcus faecalis
322 <400> SEQUENCE: 20
323 attactaca aaacaaaat cacagaagca ggccaa 36
326 <210> SEQ ID NO: 21
327 <211> LENGTH: 33
328 <212> TYPE: DNA
329 <213> ORGANISM: Staphylococcus aureus
331 <400> SEQUENCE: 21
332 tcaaatcaag tacgttggtt tttaaattatt aac 33
335 <210> SEQ ID NO: 22
336 <211> LENGTH: 33
337 <212> TYPE: DNA
338 <213> ORGANISM: Enterococcus faecalis
340 <400> SEQUENCE: 22
341 gttaattttt aaaaaccaac gtacttgatt tga 33
344 <210> SEQ ID NO: 23
345 <211> LENGTH: 36
346 <212> TYPE: DNA
347 <213> ORGANISM: Staphylococcus aureus
349 <400> SEQUENCE: 23
350 gtccgttaca cttcgacaat tacgaatgaa cagcaa 36
353 <210> SEQ ID NO: 24
354 <211> LENGTH: 36
355 <212> TYPE: DNA
356 <213> ORGANISM: Enterococcus faecalis
358 <400> SEQUENCE: 24
359 ttgctgttca ttcgtaattg tcgaagtgtgta acggac 36
362 <210> SEQ ID NO: 25
363 <211> LENGTH: 34
364 <212> TYPE: DNA
365 <213> ORGANISM: Staphylococcus aureus
367 <400> SEQUENCE: 25

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/810,428

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Input Set : A:\pto_vsk.txt

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